

Docket No.: CL000927-CIP-DIV2

Serial No.: To b assigned

Inventors: Ming-Hui WEI et al.

Title: ISOLATED HUMAN KINASE PROTEINS...

1	CAGCACGAGG	AACTCCTTCT	GATCACCTGG	CCAGCTGAGG	TCAGAGTGGG
51	AGAGGCAGTG	GTTCCATTGA	AGGAGTACTC	CTAACTGTCA	GAAGCCTGGG
101	CGGTACAGAT	GGGGTGTCT	CGCTTGGGCT	GCGGGGGGTG	TTCAGTTGCC
151	CACAGTGTAT	CTCAGGGTCT	CACCAACCAT	CCAAGCATGG	TAGGCTGTGG
201	CTGGCACCCA	GGGTTGTGTG	GCTGGGGAGG	TGGTCTCCAC	AGTTCCCTCC
251	CTGCCCTCCC	AGGGCCCCCA	TCCATGCAGG	TAACCATCGA	GGATGTGCAG
301	GCACAGACAG	GCGGAACGGC	CCAATTCGAG	GCTATCATTG	AGGGCGACCC
351	ACAGCCCTCG	GTGACCTGGT	ACAAGGACAG	CGTCCAGCTG	GTGGACAGCA
401	CCCGGCTTAG	CCAGCAGCAA	GAAGGCACCA	CATACTCCCT	GGTGCTGAGG
451	CATGTGGCCT	CGAAGGATGC	CGGCGTTTAC	ACCTGCCTGG	CCCAAAACAC
501	TGGTGGCCAG	GTGCTCTGCA	AGGCAGAGCT	GCTGGTGCTT	GGGGGGGACA
551	ATGAGCCGGA	CTCAGAGAAG	CAAAGCCACC	GGAGGAAGCT	GCACTCCTTC
601	TATGAGGTCA	AGGAGGAGAT	TGGAAGGGGC	GTGTTTGGCT	TCGTAAAAAG
651	AGTGCAGCAC	AAAGGAAACA	AGATCTTGTG	CGCTGCCAAG	TTCATCCCCC
701	TACGGAGCAG	AACTCGGGCC	CAGGCATACA	GGGAGCGAGA	CATCCTGGCC
751	CGACTGAGCT	ACCCGCTGGT	CACGGGGCTG	CTGGACCAGT	TTGAGACCCG
801	CAAGACCTTC	ATCCTCATCC	TGGAGCTGTG	CTCATCCGAG	GAGCTGCTGG
851	ACCGCCTGTA	CAGGAAGGGC	GTGGTGACGG	AGGCCGAGGT	CAAGGTCTAC
901	ATCCAGCAGC	TGGTGGAGGG	GCTGCACTAC	CTGCACAGCC	ATGGCGTTCT
951	CCACTGCGGT	ATAAGCCCT	CTAACATCCT	GATGGTGCAT	CCTGCCCGGG
1001	AAGACATTAA	AATCTGCGAC	TTTGGCTTTG	CCCAGAACAT	CACCCAGCA
1051	GAGCTGCAGT	TCAGCCAGTA	CGGCTCCCCT	GAGTTCGTCT	CCCCGAGAT
1101	CATCCAGCAG	AACCTGTGTA	GCGAAGCCTC	CGACATTTGG	GCCATGGGTG
1151	TCATCTCCTA	TCTCAGCCTG	ACCTGCTCAT	CCCCATTTGC	CGGCGAGAGT
1201	GACCGTGCCA	CCCTCCTGAA	CGTCTGGAG	GGGCGCGTGT	CATGGAGCAG
1251	CCCCATGGCT	GCCCACCTCA	GCGAAGACGC	CAAAGACTTC	ATCAAGGCTA
1301	CGCTGCAGAG	AGCCCCCTCAG	GCCCCGGCTA	GTGCGGCCCA	GTGCCTCTCC
1351	CACCCCTGGT	TCTGAAATC	CATGCCCTGC	GAGGAGGCC	ACTTCATCAA
1401	CACCAAGCAG	CTCAAGTTCC	TCCTGGCCCG	AAGTCGCTGG	CAGCGTTCCC
1451	TGATGAGCTA	CAAGTCCATC	CTGGTGATGC	GCTCCATCCC	TGAGCTGTCTG
1501	CGGGGCCAC	CCGACAGCCC	CTCCCTCGGC	GTAGCCCGGC	ACCTCTGCAG
1551	GGACACTGGT	GTCTCCTCCA	GTTCTCTCTC	CTCCTCTGAC	AACGAGCTGC
1601	CCCCATTTGC	CGGGGCTAAG	TCACTGCCAC	CCTCCCCGGT	GACACACTCA
1651	CACTGTCTGC	ACCCCCGGGG	CTTCTGCGG	CCCTCGGCCA	GCCTGCCTGA
1701	GGAAGCCGAG	GCCAGTGAGC	GCTCCACCGA	GGCCCCAGCT	CCGCCTGCAT
1751	CTCCCGAGGG	TGCCGGGCCA	CGGGCGGCC	AGGGCTGCGT	GCCCCGGCAC
1801	AGCGTCATCC	GCAGCCTGTT	CTACCACCAG	GCGGGTGAGA	GCCCTGAGCA
1851	CGGGGCCCTG	GCCCCGGGGA	GCAGGCGGCA	CCCGGCCCGG	CGGCGGCACC
1901	TGCTGAAGGG	CGGCTACATT	GCGGGGGCGC	TGCCAGGCCT	GCGCGAGCCA
1951	CTGATGGAGT	CCCGCGTGCT	GGAGGAGGAG	GCCGCCAGGG	AGGAGCAGGC
2001	CACCCCTCTG	GCCAAAGCCC	CCTCATTCGA	GACTGCCCTC	CGGCTGCCTG
2051	CCTCTGGCAC	CACTTGGGCC	CCTGGCCACA	GCCACTCCCT	GGAACATGAC
2101	TCTCCGAGCA	CCCCCGCCCC	CTCCTCGGAG	GCCTGCGGTG	AGGCACAGCG
2151	ACTCCCTTCA	GCCCCCTCCG	GGGGGGCCCC	TATCAGGGAC	ATGGGGCACC
2201	CTCAGGGCTC	CAAGCAGCTT	CCATCCACTG	GTGGCCACCC	AGGCACTGCT
2251	CAGCCAGAGA	GGCCATCCCC	GGACAGCCCT	TGGGGGCAGC	CAGCCCCTTT
2301	CTGCCACCCC	AAGCAGGGTT	CTGCCCCCCA	GGAGGGCTGC	AGCCCCCACC
2351	CAGCAGTTGC	CCCATGCCCT	CCTGGCTCCT	TCCCTCCAGT	ATCTTGCAAA
2401	GAGGCCCCCT	TAGTACCCTC	AAGCCCCTTC	TTGGGACAGC	CCCAGGCACC
2451	CCCTGCCCTT	GCCAAAGCAA	GCCCCCATT	GGACTTAAG	ATGGGGCCTG
2501	GAGACATCTC	TCTTCTTGGG	AGGCCAAAAC	CCGGCCCCCTG	CAGTTCCCCA
2551	GGGTGAGCCT	CCCAGGCGAG	CTCTTCCCAA	GTGAGCTCCC	TCAGGTTGGG
2601	CTCCTCCCAG	GTGGGCACAG	AGCCTGGCCC	CTCCTTGAT	GCGGAGGGCT
2651	GGACCCAGGA	GGCTGAGGAT	CTGTCCGACT	CCACACCCAC	CTTGACGCGG
2701	CCTCAGGAAC	AGGTGACCAT	GCGCAAGTTC	TCCCTGGGTG	GTGCGGGGGG
2751	CTACGCAGGC	GTGGCTGGCT	ATGGCACCTT	TGCCTTTGGT	GGAGATGCAG
2801	GGGGCATGCT	GGGGCAGGGG	CCCATGTGGG	CCAGGATAGC	CTGGGCTGTG
2851	TCCAGTCCGG	AGGAGGAGGA	GCAGGAGGAG	GCCAGGCTG	AGTCCAGTCC
2901	GGAGGAGCAG	CAGGAGGCCA	GGGCTGAGAG	CCCACTGCCC	CAGGTCACTG
2951	CAAGGCCTGT	GCCTGAGGTC	GGCAGGGCTC	CCACCAGGAG	CTCTCCAGAG
3001	CCCACCCCAT	GGGAGGACAT	CGGGCAGGTC	TCCCTGGTGC	AGATCCGGGA
3051	CCTGTACAGT	GATGCGGAGG	CGGCCGACAC	AATATCCCTG	GACATTTCCG
3101	AGGTGGACCC	CGCTACCTC	AACCTCTCAG	ACCTGTACGA	TATCAAGTAC
3151	CTCCCCTTCG	AGTTTATGAT	CTTCAGGAAA	GTCCCAAGT	CCGCTCAGCC
3201	AGAGCCGCCC	TCCCCATGG	CTGAGGAGGA	GCTGGCCGAG	TTCCCGGAGC
3251	CCACGTGGCC	CTGGCCAGGT	GAACTGGGCC	CCCACGCAGG	CCTGGAGATC
3301	ACAGAGGAGT	CAGAGGATGT	GGACGCGCTG	CTGGCAGAGG	CTGCCGTGGG
3351	CAGGAAGCGC	AAGTGGTCCT	CGCCGTACCG	CAGCCTCTTC	CACCTCCCTG
3401	GGAGGCACCT	GCCGCTGGAT	GAGCCTGCAG	AGCTGGGGCT	GCGTGAGAGA
3451	GTGAAGGCCT	CCGTGGAGCA	CATCTCCCGG	ATCCTGAAGG	GCAGGCCGGA

FIGURE 1A

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```
3501 AGGTCTGGAG AAGGAGGGGC CCCCAGGAA GAAGCCAGGC CTGTCTTCTT
3551 TCCGGCTCTC AGGTCTGAAG AGCTGGGACC GAGCGCCGAC ATTCCTAAGG
3601 GAGCTCTCAG ATGAGACTGT GGTCTGGGAC CAGTCAGTGA CACTGGCCTG
3651 CCAGGTGTCA GCCCAGCCAG CTGCCCAGGC CACCTGGAGC AAAGACGGAG
3701 CCCCCCTGGA GAGCAGCAGC CGTGTCTCTA TCTCTGCCAC CCTCAAGAAC
3751 TTCCAGCTTC TGACCATCCT GGTGGTGGTG GCTGAGGACC TGGGTGTGTA
3801 CACCTGCAGC GTGAGCAATG CGCTGGGGAC AGTGACCACC ACGGGCGTCC
3851 TCCGGAAGGC AGAGCGCCCC TCATCTTCGC CATGCCCGGA TATCGGGGAG
3901 GTGTACGCGG ATGGGGTGCT GCTGGTCTGG AAGCCCGTGG AATCCTACGG
3951 CCCTGTGACC TACATTGTGC AGTGCAGCCT AGAAGGCGGC AGCTGGACCA
4001 CACTGGCCTC CGACATCTTT GACTGCTGCT ACCTGACCAG CAAGCTCTCC
4051 CGGGGTGGCA CCTACACCTT CCGCACGGCA TGTGTCTAGCA AGGCAGGAAT
4101 GGTGCTCCAG ACAGACCCCT CGGAGCAAGT CCTCTGGGA GGGCCCAGCC
4151 ACCTGGCCTC TGAGGAGGAG AGCCAGGGGC GGTGAGCCCA ACCCCTGCCC
4201 AGCACAAAGA CCTTCGCATT CCAGACACAG ATCCAGAGGG GCGCTTCAG
4251 CGTGGTGCGG CAATGCTGGG AGAAGGCCAG CGGGCGGGCG CTGGCCGCCA
4301 AGATCATCCC CTACCACCCC AAGGACAAGA CAGCAGTGCT GCGCAATAC
4351 GAGGCCCTCA AGGGCCTGCG CCACCCGCAC CTGGCCAGC TGCACGCAGC
4401 CTACCTCAGC CCCCAGCACC TGGTGTCTAT CTTGGAGCTG TGCTCTGGGC
4451 CCGAGCTGCT CCCCTGCCTG GCCGAGAGGG CCTCTACTC AGAATCTGAG
4501 GTGAAGGACT ACCTGTGGCA GATGTTGAGT GCCACCCAGT ACCTGCACAA
4551 CCAGCACATC CTGCACCTGG ACCTGAGGTC CGAGAACATG ATCATCACCG
4601 AATACAACTT GCTCAAGGTC GTGGACCTGG GCAATGCACA GAGCCTCAGC
4651 CAGGAGAAGG TGCTGCCCTC AGACAAGTTC AAGGACTACC TAGAGACCAT
4701 GGTCTCCAGG TCCTTGGAGG GCCAGGGGGC TGTTCACAG ACAGACATCT
4751 GGGCCATCGG TGTGACAGCC TTCATCATGC TGAGCGCCGA GTACCCGGTG
4801 AGCAGCGAGG GTGCACGCGA CCTGCAGAGA GGACTGCGCA AGGGGCTGGT
4851 CCGGCTGAGC CGCTGTCTAG CGGGGCTGTC CGGGGGCGCC GTGGCCTTCC
4901 TGCACAGCAC TCTGTGCGCC CAGCCCTGGG GCCCGGCCCT GCGCTCCAGC
4951 TGCCTGCAGT GCGCGTGGCT AACAGAGGAG GGCCCGGCCT GTTCGCGGCC
5001 CCGCGCCGTG ACCTTCCTTA CCGCGCGGCT GCGCGTCTTC GTGCGCAATC
5051 GCGAGAAGAG ACGCGCGCTG CTGTACAAGA GGCACAACCT GGCCAGGTG
5101 CGCTGAGGGT CGCCCCGGCC ACACCCTTGG TCTCCCGCT GGGGGTCTCT
5151 GCAGACGCGC CAATAAAAC GCACAGCCGG GCGAGAAAAA AAAAAAAAAA
5201 AAAAAAA (SEQ ID NO:1)
```

FEATURES:

Start: 109

Stop: 5104

Homologous proteins:

Top BLAST Hits:

	Score	E
gi 7242949 dbj BAA92535.1  (AB037718) KIAA1297 protein [Homo sa...	425	e-117
gi 8928460 sp O75962 TRIO_HUMAN TRIPLE FUNCTIONAL DOMAIN PROTEI...	229	1e-58
gi 6005922 ref NP_009049.1  triple functional domain (PTPRF int...	229	1e-58
gi 3024081 sp Q15746 KMLS_HUMAN MYOSIN LIGHT CHAIN KINASE, SMOO...	206	2e-51
gi 90103 pir A41674 myosin-light-chain kinase (EC 2.7.1.117), ...	205	4e-51
gi 7239696 gb AAC18423.2  (U48959) myosin light chain kinase [H...	204	6e-51
gi 7239698 gb AAD15921.2  (AF069601) myosin light chain kinase ...	204	6e-51
gi 1103677 emb CAA62378.1  (X90870) myosin-light-chain kinase [...	204	6e-51
gi 3024085 sp Q28824 KMLS_BOVIN MYOSIN LIGHT CHAIN KINASE, SMOO...	203	1e-50
gi 2851405 sp P29294 KMLS_RABBIT MYOSIN LIGHT CHAIN KINASE, SMOO...	203	1e-50
gi 3982821 gb AAC83683.1  (AF081663) myosin light chain kinase ...	198	3e-49
gi 3982823 gb AAC83684.1  (AF081664) myosin light chain kinase ...	198	3e-49
gi 3982827 gb AAC83686.1  (AF081666) myosin light chain kinase ...	198	3e-49
gi 3982807 gb AAC83676.1  (AF081656) myosin light chain kinase ...	198	3e-49

BLAST dbEST hit:

gi|7958129 /dataset=dbest /taxon=960...

1283 0.0

EXPRESSION INFORMATION FOR MODULATORY USE:

From BLAST dbEST hit:

gi|7958129 Human Colon carcinoma

From PCR-based tissue screening panels:

Human Placenta

Human Kidney

Human Lung

Human skeletal muscle

Human heart

Human fetal whole brain

FIGURE 1B

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1  MGCCRLGCGG  CSAHVSQSG  LTNHPSMVGC  GWHPLGCGWG  GGLHSSLPAL
51  PGPPSMQVTI  EDVQAQTGGT  AQFEAIIEGD  PQPSVTWYKD  SVQLVDSTRL
101  SQQEGTITYS  LVLRHVASKD  AGVYTCLAQN  TGGQVLCKAE  LLVLGGDNEP
151  DSEKQSHRRK  LHSFYEVKEE  IGRGVFGFVK  RVQHKGNKIL  CAAKFIPLRS
201  RTRAQAYRER  DILAALSHPL  VTGLLDQFET  RKTLLILELE  CSSEELDLRL
251  YRKGVTTEAE  VKVYIQQQLE  GLHYLHSHGV  LHLDIKPSNI  LMVHPAREDI
301  KICDFGFAQN  ITPAELQFSQ  YGSPFVSPE  IIQNPVSEA  SDIWMGVIS
351  YLSLTCSPPF  AGESDRATLL  NVLEGRVSW  SPMAAHLSED  AKDFIKATLQ
401  RAPQARPSAA  QCLSHPWFLK  SMPAEAHFI  NTKQLKFLA  RSRWQRSLMS
451  YKSILVMRSI  PELLRGPPDS  PSLGVARHLC  RDTGSSSSSS  SSSDNELAPF
501  ARAKSLPPSP  VTHSPLLHPR  GFLRPSASLP  EEAEASERST  EAPAPPASPE
551  GAGPPAAGC  VPRHSVIRSL  FYHQAGESPE  HGALAPGSRR  HPARRRHLLK
601  GGYIAGALPG  LREPLMEHRV  LEEEAAREEQ  ATLLAKAPSF  ETALRLPASG
651  THLAPGHS  LEHDSPTPR  PSSEACGEAQ  RLPSAPSGGA  PIRDMGHPQG
701  SKQLPSTGGH  PGTAQPERPS  PDSWPQGPAP  FCHPKQGSAP  QEGCSPHAPV
751  APCPPGSFPF  GSCKEAPLVP  SSPFLGQPQA  PPAPAKASPP  LDSKMGPGDI
801  SLPGRPKPGP  CSSPGSASQA  SSSQVSSLRV  GSSQVGTEPG  PSLDAEGWTQ
851  EAEDLSDSTP  TLQRPQEQVT  MRKFSLGGRG  GYAGVAGYGT  FAFGGDAGGM
901  LGQGPWMARI  AWAVSQSEEE  EQEAREAESQ  SEEQEARAE  SPLPQVSARP
951  VPEVGRAPTR  SSPEPTPWED  IGQVSLVQIR  DLSGDAEAD  TISLDISEVD
1001  PAYLNLSLY  DIKYLPEFEM  IFRKVPKSAQ  PEPPSPMAEE  ELAEFPEPTW
1051  PWGELGPHA  GLEITEESD  VDALLAEAAV  GRKRKWSPPS  RSLFHFPGRH
1101  LPLDEPAELG  LRERVKASVE  HISRLKGRP  EGLEKEGPPR  KKPGLASFRL
1151  SGLKSWDRAP  TFLRELSDET  VVLGQSVTLA  CQVSAQPAQA  ATWSKDGAPL
1201  ESSSRVLISA  TLKNFQLTI  LVVVAEDLGV  YTCVSNALG  TVTTTGVLRK
1251  AERPSSSPCP  DIGEVYADGV  LLVWKPVESY  GPVTYIVQCS  LEGGSWTTLA
1301  SDIFDCCYLT  SKLSRGTYT  FRTACVSKAG  MGPYSSPSEQ  VLLGGPSHLA
1351  SEESQGRSA  QPLPSTKTFA  FQTQIQGRF  SVVRQCWEKA  SGRALAAKII
1401  PYHPKDKTAV  LREYEALKGL  RHPHLAQLHA  AYLSRHLVL  ILELCSPGEL
1451  LPCLAERASY  SESEVKDYLV  QMSATQYLH  NQHILHLDLR  SENMIITEYN
1501  LLKVVDLGN  QSLSQEKVLP  SDKFKDYLET  MAPELLEGQG  AVPQTDIWI
1551  GVTAFIMLSA  EYFVSSEGAR  DLQRGLRKL  VRLSRCYAGL  SGGAVAFRLS
1601  TLCAQPWGRP  CASSCLQCPW  LTEEGPACSR  PAPVTFPTAR  LRVFVRNREK
1651  RRALLYKRHN  LAQVR (SEQ ID NO:2)

```

**FEATURES:**

**Functional domains and key regions:**

**Prosite results:**

[1] PDOC00001 PS00001 ASN\_GLYCOSYLATION  
N-glycosylation site

1005-1008 NLS

---

[2] PDOC00004 PS00004 CAMP\_PHOSPHO\_SITE  
cAMP- and cGMP-dependent protein kinase phosphorylation site

Number of matches: 2

1 872-875 RKFS  
2 1084-1087 RKWS

---

[3] PDOC00005 PS00005 PKC\_PHOSPHO\_SITE  
Protein kinase C phosphorylation site

Number of matches: 23

1 97-99 STR  
2 152-154 SEK  
3 156-158 SHR  
4 230-232 TRK  
5 364-366 SDR  
6 450-452 SYK  
7 536-538 SER  
8 588-590 SRR  
9 668-670 TPR  
10 762-764 SCK  
11 827-829 SLR  
12 870-872 TMR  
13 947-949 SAR  
14 1147-1149 SFR

FIGURE 2A

15 1203-1205 SSR  
16 1211-1213 TLK  
17 1310-1312 TSK  
18 1320-1322 TFR  
19 1365-1367 STK  
20 1391-1393 SGR  
21 1434-1436 SPR  
22 1521-1523 SDK  
23 1638-1640 TAR

---

[4] PDOC00006 PS00006 CK2 PHOSPHO\_SITE  
Casein kinase II phosphorylation site

Number of matches: 21

1 59-62 TIED  
2 163-166 SFYE  
3 242-245 SSEE  
4 257-260 TEAE  
5 312-315 TPAE  
6 459-462 SIPE  
7 491-494 SSSD  
8 493-496 SDNE  
9 528-531 SLPE  
10 762-765 SCKE  
11 915-918 SQSE  
12 929-932 SQSE  
13 917-920 SEEE  
14 1351-1354 SEEE  
15 915-918 SQSE  
16 929-932 SQSE  
17 961-964 SSPE  
18 966-969 TPWE  
19 997-1000 SEVD  
20 1336-1339 SPSE  
21 917-920 SEEE

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[5] PDOC00008 PS00008 MYRISTYL  
N-myristoylation site

Number of matches: 27

1 7-12 GCGGCS  
2 10-15 GCSVAH  
3 41-46 GGLHSS  
4 42-47 GLHSSL  
5 106-111 GTTYSL  
6 122-127 GVYTCL  
7 133-138 GQVLCK  
8 484-489 GGSSSS  
9 485-490 GSSSSS  
10 601-606 GGYIAG  
11 606-611 GALPGL  
12 708-713 GGHPGT  
13 877-882 GGRGGY  
14 880-885 GGYAGV  
15 894-899 GGDAGG  
16 898-903 GGMLGQ  
17 1061-1066 GLEITE  
18 1174-1179 GQSVTL  
19 1229-1234 GVYTCS  
20 1240-1245 GTVTTT  
21 1293-1298 GGSWTT  
22 1294-1299 GSWTTL  
23 1316-1321 GGTYYTF  
24 1508-1513 GNAQSL  
25 1575-1580 GLRKGL  
26 1589-1594 GLSGGA  
27 1592-1597 GGAVAF

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FIGURE 2B

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[6] PDOC00009 PS00009 AMIDATION

Amidation site

1080-1083 VGRK

[7] PDOC00373 PS00343 GRAM\_POS\_ANCHORING

Gram-positive cocci surface proteins 'anchoring' hexapeptide

704-709 LPSTGG

[8] PDOC00100 PS00107 PROTEIN\_KINASE\_ATP

Protein kinases ATP-binding region signature

171-194 IGRGVFGFVKRVQHKGNKILCAAK

[9] PDOC00100 PS00108 PROTEIN\_KINASE\_ST

Serine/Threonine protein kinases active-site signature

280-292 VLHLDIKPSNILM

[10] PDOC00100 PS00109 PROTEIN\_KINASE\_TYR

Tyrosine protein kinases specific active-site signature

1484-1496 ILHLDLRSENMII

[11] PDOC00565 PS00659 GLYCOSYL\_HYDROL\_F5

Glycosyl hydrolases family 5 signature

142-151 LVLGGDNEPD

BLAST Alignment to Top Hits:

>gi|7242949|dbj|BAA92535.1| (AB037718) KIAA1297 protein [Homo sapiens]  
Length = 2242

Score = 425 bits (1081), Expect = e-117

Identities = 305/876 (34%), Positives = 423/876 (47%), Gaps = 106/876 (12%)

Query: 54 PSMQVTIEDVQAQTGGTAQFEAIIIEGDPQPSVTWYKDSVQLVDSTRLSQQQEGTTSYSLVL 113  
P + +EDV+ G TA+F ++EG P P + WYKD V L +S+ +S E SLV+  
Sbjct: 504 PRFESIMEDVEVGAGETARFAVVVEGKPLPDIMWYKDEVLLTESSHVSFVYEENECSLVV 563

Query: 114 RHVASKDAGVYTCLAQNTGGQVLCKAELLVLGGDN---EPDSEKQSHR-RKLHSFYEVK 168  
++D GVYTC AQN G+V CKAE L V E E + HR R+L FY++  
Sbjct: 564 LSTGAQDGGVYTCTAQNLAGVSCKAELAVHSAQTAMEVEGVEDEHRRRLSDFYDIH 623

Query: 169 EEIGRGVFGFVKRVQHKGNKILCAAKFIPLRSRTRAQAYRERDILAALSHPLVTGLLDQF 228  
+EIGRG F +++R+ + + + AAKFIP +++ +A A RE +LA L H V + F  
Sbjct: 624 QEIGRGAFSYLRRIVERSSSGLEFAAKFIPSAKPKASARREARLLARLQHDVCVLYFHEAF 683

Query: 229 ETRKTLILILELCSSEELLDRLYRKGVVTEAEVKVYIQQQLVEGLHYLHSHGVLHLDIKPS 288  
E R+ L+++ ELC+ EELL+R+ RK V E+E++ Y++Q++EG+HYLH VLHLD+KP  
Sbjct: 684 ERRRGLVIVTELCT-EELLERIARKPTVCESEIRAYMRQVLEGIHYLHQSHVLHLDVKPE 742

Query: 289 NILMVHPA--REDIKICDFGFAQNITPAELQFSQYGSPEFVSPEIIQNPVSEASDIWAM 346  
N+L+ A + ++ICDFG AQ +TP E Q+ QYG+PEFV+PEI+ Q+PVS +DIW +  
Sbjct: 743 NLLVWDGAAGEQQVRICDFGNAQELTPGEPQYCQYGTPEFVAPEIVNQSPVSGVTDIWPV 802

Query: 347 GVISYLSLTCSSPFAGESDRATLLNVLEGRVSWSSPMAHLSEDAKDF-IKATLQRAPQA 405  
GV+++L LT SPF GE+DR TL+N+ V++ LS +A+ F IK +Q +  
Sbjct: 803 GVVAFCLCTGISPFVGENDRITLMNIRYNVAFETTFLSLSREARGFLIKVLVQ--DRL 860

Query: 406 RPSAAQCLSHPWFLKSMPEAEAHFINTKQLKFLARSRWQSLMSYKSILVMRSIPELLR 465  
RP+A + L HPWF E ++T LK L+R RWQRS +SYK LV+R IPELLR  
Sbjct: 861 RPTAETLEHPWFKTQAKGAE---VSTDHLKFLSRRRWQRSQISYKCHLVLRPIPELLR 917

Query: 466 GPPDSPSLGVARHLCRDTGGSSSSSSSSSDNELAPFARAK-----SLPPSPVTH 513  
PP+ + + R +GG SSSS S + EL SL P  
Sbjct: 918 APPERVVWTPRR-PPPSGGLSSSSDSEEELEELPSVPRPLQPEFSGSRVSLTDIPTED 976

Query: 514 SPLHLPRGFLRPSASLPPEAEASERSTEAPAPPASPEGAGPPAAQGCVPRHSVI----- 567

FIGURE 2C

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L P E+ A + EAP+P A P PAA G PR +  
Sbjct: 977 EALGTPETGAATPMDWQEQGRAPSDQDEAPSPEALPSPGQEPAA-GASPRRGELRRGSSA 1035  
Query: 568 -----RSLFYHQAGESPEHGALAPG-----SRRHPARRRHLLK 600  
R L + E P+ + PG ++R A R+ LL+  
Sbjct: 1036 ESALPRAGPRELGRGLHKAASVELPQRRSPGPGATRLARGGLGEGEYAQRLQALRQRLLR 1095  
Query: 601 GGYIAGALPGLREPLMEH-----RVLEEEAAREEQATL----LAKAPSFETALR 645  
GG G + GLR PL+E R EAA Q L L K+ SF  
Sbjct: 1096 GGPEDGKVSGLRGPLLESGLGRARDPRMARASSEAAPHHPPLENRGLQKSSSFSQGEA 1155  
Query: 646 LPASGTHLAPGHSLSLEHDSPTPR----PSSEACGEAQLPSAPSGGAPIRDMGHPQGS 701  
P G H G + R PS A EAQ PS+P+ P  
Sbjct: 1156 EP-RGRHRRAGAPLEIPVARLGARRIQESPSSLSEALSEAQ--PSSPA-----RPSAP 1203  
Query: 702 KQLPSTGGHPGTAQPERPSPDPSWGPQAPFCHPKQGSAPQEGCSHPAVAPCPP----GS 757  
K PST P +A+P +P PAP P Q AP+ P A P PP +  
Sbjct: 1204 K--PST---PKSAEPSATTPSDAPQPPAP--QPAQDKAPEPRPEPVRASKPAPPPQALQT 1256  
Query: 758 FPPGSKCEAPLVPSFPFLGQPQAPPAPAKASPLDSKMGPGDISLPGRPKPGPCSSPGSA 817  
A ++ S G Q P+ A+PP + K + P PG +  
Sbjct: 1257 LALPLTPYAQIIQSLQLSGHAQG-PSQGPAAAPPSEPKPHAAVFARVASPPPG--APEKRV 1313  
Query: 818 SQASSSQVSSLRVGSSQVGTEPGPSLDAEGWTQEA 853  
A V + + V PG SL + E+E  
Sbjct: 1314 PSAGGPPVLAEKARVPTVPPRPGSSSLSSSIENLESE 1349 (SEQ ID NO:4)

Score = 210 bits (529), Expect = 1e-52

Identities = 111/281 (39%), Positives = 156/281 (55%), Gaps = 2/281 (0%)

Query: 1336 SPSEQVLGGPSHLASEEESQGRSAQPLPSTKTFAFQTQIQGRFVSVRQCWEKASGRAL 1395  
SP+++V+ S S +G ++ P K + F + RGRF VVR C E A+GR  
Sbjct: 1952 SPAKEVSSSPGSSPRSSPRPEGTTLRQGPQKPYTFLEEKARGRFGVVRACRENATGRTF 2011  
Query: 1396 AAKIIPYHPKDKTAVLREYEALKGLRHPHLAQLHAAYLSPRHLVLILELCSGPELLPCLA 1455  
AKI+PY + K VL+EYE L+ L H + LH AY++PR+LVLI E C ELL L+  
Sbjct: 2012 VAKIVPYAAEGKPRVLQEQYEVLRTHLHERIMSLHEAYITPRYLVLIAESCGNRELLCGLS 2071  
Query: 1456 ERASYSESEVKDYLMQMSLATQYLHNQHILHLDLRSENMIITEYNLLKVVDLGNAQSLSQ 1515  
+R YSE +V Y+ Q+L YLH H+LHLD++ +N+++ N LK+VD G+AQ +  
Sbjct: 2072 DRFRYSEDDVATYMVQLLQGLDYLGHHVHLHLDIKPDNLLAPDNALKIVDFGSAQPYNP 2131  
Query: 1516 EKVLPSPDKFKDYLETMAPELLEGQGAVPQTDIWAIGVTAFIMLSAEYPVSSEGARDLQRG 1575  
+ + P LE MAPE+++G+ TDIW GV +IMLS P ++ +  
Sbjct: 2132 QALRPLGHRTGTLEFMAPEMVKGEPIGSATDIWGAGVLTYYIMLSGRSPFYEPDPQETEAR 2191  
Query: 1576 LRKGLVRLSRCYAGLSGGAVAFLRSTLCAQPWGRPCASSCL 1616  
+ G + Y S A FLR L PW RP SSCL  
Sbjct: 2192 IVGGRFADFQLYPNTSQSATLFLRKVLSVHPWSRP--SSCL 2230 (SEQ ID NO:5)

Score = 170 bits (426), Expect = 1e-40

Identities = 168/574 (29%), Positives = 256/574 (44%), Gaps = 42/574 (7%)

Query: 1103 LDEP--AELGLRERVKASVEHISRLKGRPEGLEKEGPPRKKPGLASFRLSGLKSWDRAP 1160  
L EP A GLR+ V+HI R+L + K PP + L L + + AP  
Sbjct: 358 LREPGWAATGLRK----GVQHIFRVLSTTVKSSSKPSPSEPVLQ----LEHGPTLEEAP 409  
Query: 1161 TFLRELSDETIVVLGQSVTLACQVSAQPAQATW-SKDGAPLESSSRVL-ISATLKNFQLL 1218  
L + VV GQ ++ + AQ W S GA LE+ + V +S + L  
Sbjct: 410 AMLDKPDIVYVVEGQPASVTVTFN-HVEAQVVWRSCRGALLEARAGVYELS QPDDDDQYCL 468  
Query: 1219 TILVVVAEDLGVTCSVSNALGTVTTTGVLRKAERPS-SSPCPI----GEVYADGVLLV 1273  
I V D+G TC+ N GT T + L AE P S D+ GE V++  
Sbjct: 469 RICRVSRRDMGALTCTARNRHGTQTCSTVLELAEAPRFESIMEDVEVGAGETARFAVVVE 528  
Query: 1274 WKPVESYGPVTYIVQCSLEGGSWTTLASDIFDCCY--LTSKLSRGGTYTFRACVSKAGM 1331  
KP+ + Y + L S + + +C L++ GG YT C ++  
Sbjct: 529 GKPLPDI--MWYKDEVLLTESSHVSFVYEEENECSLVVLSTGAQDGGVYT----CTAQNLA 582

FIGURE 2D

Docket No.: CL000927-CIP-DIV2  
Serial No.: To be assigned  
Inventors: Ming-Hui WEI et al.  
Title: ISOLATED HUMAN KINASE PROTEINS...

Query: 1332 GPYSSPSEQVLLGGPSHLASEEESQGRSAQPLPSTKTFAFQTQIQGRFSVVRQCWEKAS 1391  
G S +E + + + E + + + + +I RG FS +R+ E++S  
Sbjct: 583 GEVSCKAELAVHSAQTAMEVEGVGEDEDHRGRRLSDFYDIHQEIGRGAFSYLRRIVERSS 642

Query: 1392 GRALAAKIIPYHPKDKTAVLREYEALKGLRHPHLAQLHAAYLSPRHLVLILELCSGPELL 1451  
G AAK IP K K + RE L L+H + H A+ R LV++ ELC+ ELL  
Sbjct: 643 GLEFAAKFIPSQAKPKASARREARLLARLQHDCLVLFHEAFERRRGLVIVTELCT-EELL 701

Query: 1452 PCLAERASYSESEVKDYWLQMLSATQYLHNQHILHLDLRSNMIITE----YNLLKVVDL 1507  
+A + + ESE++ Y+ Q+L YLH H+LHLD++ EN+++ + + + D  
Sbjct: 702 ERIARKPTVCESEIRAYMRQVLEGIHYLHQSHVLHLDVLPENLLVWDGAGEQQVRICDF 761

Query: 1508 GNAQSLSQEKVLPSPDKFKDYLETMAPELLEGQGAVPQTDIWAIGVTAIFIMLSAEYPVSSE 1567  
GNAQ L+ + P E +APE++ TDIW +GV AF+ L+ P E  
Sbjct: 762 GNAQELTPGE--PQYCYGTPEFVAPAEIVNQSPVSGVTDIWPVGVVAFCLCTGISPFVGE 819

Query: 1568 GARDLQRLRGLRGLVRLSR-CYAGLSGGAVAFRLSTLCAQPWGRPCASSCLQCPWLTEEGP 1626  
R +R V + LS A FL L Q RP A L+ PW +  
Sbjct: 820 NDRITLMNIRNYNVAFEETFLSLSRREARGFLIKVL-VQDRLRPTAEETLEHPWFKTQ-- 876

Query: 1627 ACSRPAPVTFPTARLRVFFV-RNREKRRALLYKRH 1659  
++ A V+ T L++F+ R R +R + YK H  
Sbjct: 877 --AKGAEVS--TDHLKLFLSRRRWQRSQISYKCH 906 (SEQ ID NO:6)

Score = 145 bits (362), Expect = 4e-33  
Identities = 85/253 (33%), Positives = 135/253 (52%), Gaps = 5/253 (1%)

Query: 165 YEVKEEIGRGVGFVKRVQHKGNILCAAKFIPLRSRTAQAYRERDILAALSHPLVTGL 224  
Y EE RG FG V+ + AK +P + + + +E ++L L H + L  
Sbjct: 1985 YTFLEEKARGRFGVVRACRENATGRFTVAKIVPYAAEGKPRVLQYEYEVLRTLHHERIMSL 2044

Query: 225 LDQFETRKTLLILELCSSEELLDRLYRKGVVTEAEVKVYIQLVEGLHYLHSHGVHLHD 284  
+ + T + L+LI E C + ELL L + +E +V Y+ QL++GL YLH H VLHLD  
Sbjct: 2045 HEAYITPRYLVLIAESCGNRELLCGLSDRFRYSEDDVATYMQLLQGLDYLGHHVHLHD 2104

Query: 285 IKPSNIMVHPAREDIKICDFGFAQNITPAELQ--FSQYGSPEFVSPEIIQONPVSEASD 342  
IKP N+L+ +KI DFG AQ P L+ + G+ EF++PE+++ P+ A+D  
Sbjct: 2105 IKPDNLLLA--PDNALKIVDFGSAQYPNPQALRPLGHRTGTLEFMAPEMVKGEPISATD 2162

Query: 343 IWAMGVISYLSLTSSPFAGESDRATLLNVLEGRVSWSSPMAAHLSEDAKFIKATLQRA 402  
IW GV++Y+ L+ SPF + T ++ GR + + + S+ A F++ L  
Sbjct: 2163 IWGAGVLTYIMLSGRSPFYEPDPQETEARIVGGRFD-AFQLYPNTSQSATLFLRKVLSVH 2221

Query: 403 PQARPSAAQCLSH 415  
P +RPS+ + H  
Sbjct: 2222 PWSRPSSCLSVCH 2234 (SEQ ID NO:7)

Score = 128 bits (319), Expect = 4e-28  
Identities = 81/245 (33%), Positives = 120/245 (48%), Gaps = 19/245 (7%)

Query: 1139 PRKKPGLASFRLSGL-----KSWDRAPTFLRELSDETIVLGQSVTLACQVSAQP 1187  
PRK GL+ LS D P F +L D+ ++ G++ TL C +A P  
Sbjct: 1571 PRKDKGLSPPNLSASVQEELGHQYVRSESDFPFVFIKLKDQVLEGEAATLLCLPAACP 1630

Query: 1188 AAQATWSKDGAPLESSSRVLISATLKNFQLLTILVVVAEDLGVTCSVSNALGTVTTTGV 1247  
A +W KD L S V+I + QLL+I G+Y CS +N LG++T++  
Sbjct: 1631 APHISWMKDKSLRSEPSVIIVSCKDGRQLLSIPRAGKRHAGLYECSATNVLSITSSCT 1690

Query: 1248 LRKAERPSSSPCPDIGEVYADGVLLVWKPVESYGPVTYIVQCSLEGGG-WTTLASDIFDC 1306  
+ A P P++ + Y D L++WKP +S P TY ++ ++G S W ++S I DC  
Sbjct: 1691 VAVARVPGKLAPPEVTQTYQDTALVLWKPGRSAPCTYTLERRVDGESVWHFVSSGIPDC 1750

Query: 1307 CYLTSKLSRGGTYTFRACVSKAGMPYSSPSEQVLLGG-----PSHLASEEESQGRS 1359  
Y + L G T FR AC ++AG GP+S+ SE+V + G PS E R  
Sbjct: 1751 YYNVTHLPVGVTVRFRVACANRAGQGPFSNSSEKVFVRGTQDSSAVPSAAHQEAPVTSRP 1810

Query: 1360 AQPLP 1364

FIGURE 2E

Docket No.: CL000927-CIP-DIV2  
Serial No.: To be assigned  
Inventors: Ming-Hui WEI et al.  
Title: ISOLATED HUMAN KINASE PROTEINS...

A+ P  
Sbjct: 1811 ARARP 1815 (SEQ ID NO:8)

Score = 71.0 bits (171), Expect = 9e-11  
Identities = 41/115 (35%), Positives = 57/115 (48%), Gaps = 4/115 (3%)

Query: 60 IEDVQAQTGGTAQFEAIEGDPQPSVTWYKDSVQLVDSTRLSQQQEGTTYSLVLRHVASK 119  
+EDV+ G A+F+ I G P P VTW + +S L +Q+G +SL + HV S+  
Sbjct: 89 LEDVEVLEGRAARFDCKISGTPPPVVTWTHFGCPMEESNLRLRQDGGGLHSLHIAHVGSE 148

Query: 120 DAGVYTCLAQNTGGQVLCKAELLVLGGDNEPDSEKQSHRRKLHSFYEVKEEIGRG 174  
D G+Y A NT GQ C A+L V EP + KL + EE +G  
Sbjct: 149 DEGLYAVSAVNTHGQAHCSAQLYV----EEPRTAASGPSSKLEKMPISPEEPEQG 199 (SEQ ID NO:9)

Score = 60.1 bits (143), Expect = 2e-07  
Identities = 54/199 (27%), Positives = 81/199 (40%), Gaps = 12/199 (6%)

Query: 1160 PTFLELSDETIVVLGQSVTLACQVSAQPAQATWSKDGAPLESSSRVLISATLKNFQLLT 1219  
P FLR L D V L + L CQV+ P +W +G ++SS ++ ++ L  
Sbjct: 207 PDFLRPLQDLEVLGAKEAMLECCQVTGLPYPTISWFHNGHRIQSSDDRRMT-QYRDVHRLV 265

Query: 1220 ILVVVAEDLGVYTCSVSNALGTVTTTGVLRKAERPSSSP--CPDIGEVYADGVLLVWKPV 1277  
V + GYV ++N LG L + P P + V V L W P  
Sbjct: 266 FPAVGPQHAGVYKSVIANKLGAACYAHLYVTDVVPGPDPGAPQVAVTGRMVTLTWNPP 325

Query: 1278 ESY-----GPVTYIVQCSLEGG-SWTTLASDIFDCCYLTSKLSRGGTYTFRACVSKAG 1330  
S +TY VQ + G WT L + + + + + L +G + FR +  
Sbjct: 326 RSLDMAIDPDSLTYTVQHQLGSDQWTALVTGLREPGWAATGLRKGVQHIFRVLSTTVKS 385

Query: 1331 MGPYSSPSE--QVLLGGPS 1347  
S PSE Q+L GP+  
Sbjct: 386 SSKPSPSPSEPVQLLEHGPT 404 (SEQ ID NO:10)

Score = 45.7 bits (106), Expect = 0.004  
Identities = 30/102 (29%), Positives = 45/102 (43%), Gaps = 1/102 (0%)

Query: 1159 APTFLRELSDETIVVLGQSVTLACQVSAQPAQATWSKDGAPLESSSRVLISATLKNFQLL 1218  
AP F R L D V+ G++ C++S P TW+ G P+E S + + L  
Sbjct: 82 APLFTRLLEDVEVLEGRAARFDCKISGTPPPVVTWTHFGCPMEESNLRLRQD-GGLHSL 140

Query: 1219 TILVVVAEDLGVYTCSVSNALGTVTTTGVLRKAERPSSSPCP 1260  
I V +ED G+Y S N G + L E +++ P  
Sbjct: 141 HIAHVGSEDEGLYAVSAVNTHGQAHCSAQLYVEEPRTAASGP 182 (SEQ ID NO:11)

Score = 43.8 bits (101), Expect = 0.015  
Identities = 58/217 (26%), Positives = 84/217 (37%), Gaps = 23/217 (10%)

Query: 619 RVLEEEAAREEQATLLAKAPSFETALRLPASGTHLAPGHSHSLEHDSPTPRPSSEACGE 678  
R ++ +A A A S R P S T LAP + + T PSS  
Sbjct: 1788 RGTQDSSAVPSAAHQEAPVTSRPARAPPDSPPTSLAPPLAPAAPTPPSVTVPSSPPTPP 1847

Query: 679 AQRLPSPAPSGGAPIRDMGHPQGSQQLPSTGGHPGTAQPERPSPDSPWGPAPFCHPKQGS 738  
+Q L S + G P + P+ + L + A+P PS +P PF  
Sbjct: 1848 SQALSSLKAVGPPPTQTP--PRRHRLQAAR----PAEPTLPSTHVTPEPKPFVLD---- 1897

Query: 739 APQEGCSPHAPAVAPCPPGSPGSCKEAPLVPSSPFLGQPQAPPAPAKASPPLDKMGPG 798  
+ P A P G P S P+ + F+ P AP PA PP +K+  
Sbjct: 1898 -----TGTFIPASTPQGVKPVSS--STPVYVVTSFVSAPPAPEPPAPEPPPEPTKVTQV 1949

Query: 799 DISLPGRPKPGPCSSPGSASQAS-SSQVSSLRVGSSQ 834  
+S P SSPGS+ ++S + ++LR G Q  
Sbjct: 1950 SLS----PAKEVVSSPGSSPRSSPRPEGTTLRQGPPQ 1982 (SEQ ID NO:12)

Score = 43.0 bits (99), Expect = 0.026  
Identities = 25/92 (27%), Positives = 44/92 (47%), Gaps = 4/92 (4%)

FIGURE 2F



Docket No.: CL000927-CIP-DIV2  
Serial No.: To be assigned  
Inventors: Ming-Hui WEI et al.  
Title: ISOLATED HUMAN KINASE PROTEINS...

Query: 54 PSMQVTIEDVQAQTGGTAQFEAIEGDPQPSVTWYKDS--VQLVDSTRLSQQQEGTTYSL 111  
P ++D++ A E + G P P+++W+ + +Q D R++Q ++ + L  
Sbjct: 207 PDFLRPLQDLEVLAKEMLEECQVTGLPYPTISWFHNGHRIQSSDDRRMTQYRD--VHRL 264

Query: 112 VLRHVASKDAGVYTCLAQNTGGQVLCKAELLV 143  
V V + AGVY + N G+ C A L V  
Sbjct: 265 VFPAVGPPHAGVYKSVIANKLGAACYAHLV 296 (SEQ ID NO:13)

>gi|8928460|sp|O75962|TRIO\_HUMAN TRIPLE FUNCTIONAL DOMAIN PROTEIN  
(PTPRF INTERACTING PROTEIN) >gi|3644048|gb|AAC43042.1|  
(AF091395) Trio isoform [Homo sapiens]  
Length = 3038

Score = 229 bits (579), Expect = 1e-58  
Identities = 143/418 (34%), Positives = 215/418 (51%), Gaps = 11/418 (2%)

Query: 53 PPSMQVTIEDVQAQTGGTAQFEAIEGDPQPSVTWYKDSVQLVDST---RLSQQQEGTTY 109  
PP + + +V +TG T + G P+ S+TW +++ +S G  
Sbjct: 2625 PPEFVLIPLSEVTCETGETVVLRCRVCGRPKASITWKGPENHTLNNDGHYSISYSDLGAE- 2683

Query: 110 SLVLRHVASKDAGVYTCLAQNTGGQVLCKAELLVLGGDNEPDSEKQSHRRKLHSFYEVKE 169  
+L + V ++D G+YTC+A N G A L VLG D + + SFY  
Sbjct: 2684 TLKIVGVTTEDDGIYTCIAVNDMGSSASSASLRVLGPGM--DGIMVTWKDNFDSFYSEVA 2741

Query: 170 EIGRGVGFVQKRVQHKGNKILCAAKFIPLRSRTRAQAYRERDILAALSHPLVTGLLDQFE 229  
E+GRG F VK+ KG K A KF+ + R Q E IL +L HPL+ GLLD FE  
Sbjct: 2742 ELGRGRFSVVKCDQKGTKRAVATKFNKKLMKRDQVTHELGILQSLQHPLLVGLLDTFE 2801

Query: 230 TRKTLILILELCSSEELDLRLYRKGVTTEAEVKVYIQQLVLEGLHYLHSHGVLHLDIKPSN 289  
T + IL+LE+ LLD + R G +TE +++ ++ ++E + YLH+ + HLD+KP N  
Sbjct: 2802 TPTSYILVLEMAHQGRLLDCVVRWGSITTEGKIRAHLEGEVLEAVRYLHNCRIAHLDLKPEN 2861

Query: 290 ILMVHP-AREDIKICDFGFAQNITPAELQFSQYGSPEFVSPEIIQQNPVSEASDIWAMGV 348  
IL+ A+ IK+ DFG A + G+PEF +PEII NPVS SD W++GV  
Sbjct: 2862 ILVDESIAKPTIKLADFGDAVQLNTTYIYHQLLGNPEFAAPEIILGNPVSLTSDTWSVG 2921

Query: 349 ISYLSLTCSSPFAGESDRATLLNVLEGRVSWSSPMAAHLSEDAKDFIKATLQRAQARPS 408  
++Y+ L+ SPF +S T LN+ S+ +S+ AK+F+ LQ P RPS  
Sbjct: 2922 LTYVLLSGVSPFLDSDVEETCLNICRLDFSFPDDYFKGVSQKAKEFVCFLQEDPAKRPS 2981

Query: 409 AAQCLSHPWFLKSMPAEAAHFINTKQLKFLARSRWQ---RSLMSYKSILVMRSIPEL 463  
AA L W L++ ++T +L + R + Q R + S K+ L R +P +  
Sbjct: 2982 AALALQEQW-LQAGNGRSTGVLDTSRLTSFIERRKHQNDVRPIRSIKNFLQSRLLPRV 3038  
(SEQ ID NO:14)

Score = 121 bits (300), Expect = 7e-26  
Identities = 82/280 (29%), Positives = 137/280 (48%), Gaps = 10/280 (3%)

Query: 1374 QIQGRFSVVRQCWEKASGRALAAKIIPYHPKDKTAVLREYEALKGLRHPHLAQLHAAAYL 1433  
++ RGRFSV++C +K + RA+A K + + V E L+ L+HP L L +  
Sbjct: 2742 ELGRGRFSVVKCDQKGTKRAVATKFNKKLMKRDQVTHELGILQSLQHPLLVGLLDTFE 2801

Query: 1434 SPRHLVLILELCSGPELLPCLAERASYSESEVKDYLVQMLSATQYLHNQHILHLDLRSN 1493  
+P +L+LE+ LL C+ S +E +++ +L ++L A +YLHN I HLDL+ EN  
Sbjct: 2802 TPTSYILVLEMAHQGRLLDCVVRWGSITTEGKIRAHLEGEVLEAVRYLHNCRIAHLDLKPEN 2861

Query: 1494 MIITE---YNLLKVVDLGNAQSLSQEKVLPDSKFKDYLETMAPELLEGQGAVPQTDIWI 1550  
+++ E +K+ D G+A L+ + + E APE++ G +D W++  
Sbjct: 2862 ILVDESIAKPTIKLADFGDAVQLNTTYI--HQLLGNPEFAAPEIILGNPVSLTSDTWSV 2919

Query: 1551 GVTAFIMLSAEYPVSSEGARDLQRL-RKGLVRLSRCYAGLSGGAVAFRLSTLCAQPWGR 1609  
GV +++LS P + + + R + G+S A F+ L P R  
Sbjct: 2920 GVLTYVLLSGVSPFLDSDVEETCLNICRLDFSFPDDYFKGVSQKAKEFVCFLQEDPAKR 2979

Query: 1610 PCASSCLQCPWLTEEGPACSRPAPVTFPTARLRFVVRNRE 1649  
P A+ LQ WL A + + T+RL F+ R+  
Sbjct: 2980 PSAALALQEQWL---QAGNGRSTGVLDTSRLTSFIERRK 3015 (SEQ ID NO:15)

FIGURE 2G

Dock t No.: CL000927-CIP-DIV2  
Serial No.: To b assigned  
Inventors: Ming-Hui WEI et al.  
Title: ISOLATED HUMAN KINASE PROTEINS...

Score = 55.4 bits (131), Expect = 5e-06  
Identities = 42/153 (27%), Positives = 70/153 (45%), Gaps = 17/153 (11%)

Query: 1128 GRPEGLEKEGPPRKKPGLASFRLSGLKS----WDRAPTFLRELSDET VVLGQSVTLACQV 1183  
G+ EG + G + + GL++ L + +D P F+ LS+ T G++V L C+V  
Sbjct: 2590 GKREGKLENGYRKSREGLSNKVSVKLLNPNIYDVPPEFVIPLSEVTCETGETVVLRCRV 2649

Query: 1184 SAQPAAQATW-SKDGAPLESSSRVLISATLKNFQLLTILVVVAEDLGVTCSVSNALGTV 1242  
+P A TW + L + IS + L I+ V ED G+YTC N +G+  
Sbjct: 2650 CGRPKASITWKGPENHTLNNDGHYSISYSDLGATLKIVGVTTEDDGIYTCIAVNDMGSA 2709

Query: 1243 TTTGVLKRAERPSSSPCPDIGEVYADGVLLVWK 1275  
+++ LR + DG+++ WK  
Sbjct: 2710 SSSASLR-----VLGPGMDGIMVTWK 2730 (SEQ ID NO:16)

Score = 39.1 bits (89), Expect = 0.39  
Identities = 61/208 (29%), Positives = 76/208 (36%), Gaps = 65/208 (31%)

Query: 688 GGAPIRDMGHPQGSQKLPSTGGHPGTA-----QPERPSPD-----S 723  
GGAP GH G S GG P T+ QP R P S  
Sbjct: 2252 GGAPSGSGSGHSGGPS---SCGGAPSTSRSRPSRIPQVVRHPPVLVSSAASSQAEADKMS 2308

Query: 724 PWGQPAFCHPKQGSAPQEGCSPHPAVAPCPGSPFPGSCKEAPLVSSPFLGQPQ---- 779  
P P P G+AP+ G S A + PPG+ GS +EA +P L P+  
Sbjct: 2309 GTSTPGPSL-PPGAAPAEAGPS---APSRPPGADAEBSEREAEIPKMKVLESPRKGAA 2364

Query: 780 -----APPAPAK-----ASPLDSKMGPGDISLPGRPKPGPCSSPGSA 817  
+P APAK A+ PL+S + SL P P P S  
Sbjct: 2365 NASGSSPDAPAKDARASLGTLPKPRAGAASPLNSPLSSAVPSLGEKPEFP-----PSSP 2419

Query: 818 SQASSSQVSSLRVG-SSQVG--TEPGPS 842  
Q S SS+ +S+ G T PG S  
Sbjct: 2420 LQKGSFWSIPASPASRPGSFTFPGDS 2447 (SEQ ID NO:17)

>gi|3024081|sp|Q15746|KMLS\_HUMAN MYOSIN LIGHT CHAIN KINASE, SMOOTH  
MUSCLE AND NON-MUSCLE ISOZYMES (MLCK) [CONTAINS: TELOKIN]  
Length = 1913

Score = 206 bits (518), Expect = 2e-51  
Identities = 104/298 (34%), Positives = 173/298 (57%), Gaps = 2/298 (0%)

Query: 159 RKLHSFYEVKEEIGRGVFGVFKRVQHKGNKILCAAKFIPLRSRTRAQAYRER-DILAALS 217  
+K+ FY+++E +G G FG V R+ K + + A KF S + R+ I+ L  
Sbjct: 1458 QKVSDFYDIEERLGSFGKQVFRVLEKTRKVVAGKFFKAYSACEKENIRQEISIMNCLH 1517

Query: 218 HPLVTGLLDQFETRKTLLILELCSSEELDLRLYRKGV-VTEAEVKVYIQQVLEGLHYLH 276  
HP + +D FE + ++++LE+ S EL +R+ + +TE E Y++Q+ EG+ Y+H  
Sbjct: 1518 HPKLVQCVDFAFEKANIVMVLEIVSGGELFERIIDEFELTERECIKYMRQISEGVYIH 1577

Query: 277 SHGVLHLDIKPSNIMLVHPAREDIKICDFGFAQNITPAELQFSQYGSPEFVSPEIIQONP 336  
G++HLD+KP NI+ V+ IK+ DFG A+ + A +G+PEFV+PE+I P  
Sbjct: 1578 KQGIHVHLDLKPENIMCVNKTGTRIKLIDFGLARLENAGSLKVLFGTPEFVAPEVINYEP 1637

Query: 337 VSEASDIWAMGVISYLSLTCSPPFAGESDRATLLNVLEGRVSWSSPMAAHLSEDAKDFIK 396  
+S A+D+W++GVI Y+ ++ SPF G++D TL NV + +S+DAKDFI  
Sbjct: 1638 ISYATDMWSIGVICIYLVSLSPFMGDNDNETLANVTSATWDFDDEAFDEISDDAKDFIS 1697

Query: 397 ATLQRAPQARPSAAQCLSHPWFLKSMPAEEAHFINTKQLKFLARSRWQRLMSYKSI 454  
L++ + R QCL HPW +K EA ++ ++K +AR +WQ++ + ++I  
Sbjct: 1698 NLLKKDMKNRLDCTQCLQHPWLMKDTKNMEAKKLSKDRMKKYMARRKWQKTGNVRAI 1755  
(SEQ ID NO:18)

Score = 127 bits (315), Expect = 1e-27  
Identities = 134/528 (25%), Positives = 219/528 (41%), Gaps = 55/528 (10%)

Query: 1132 GLEKEGPPRKKPGLASFRLSGLKSWDRAPTFLRELSDET VVLGQSVTLACQVSAQPAAQA 1191  
G E + +KKP + + + P ++ D+ V G+SV L +V+  
Sbjct: 1215 GTESDATVKKKPAKTPPKAAMP-----PQIIQFPEDQKVRAGESVELFGKVTGTQPITC 1269

FIGURE 2H

Dock t No.: CL000927-CIP-DIV2  
 S rial No.: To be assigned  
 Inventors: Ming-Hui WEI et al.  
 Title: ISOLATED HUMAN KINASE PROTEINS...

Query: 1192 TWSKDGAPLESSSRVLISATLKNFQLLTILVVVAEDLGVTYCSVSNALGT---VTTTGV 1247  
 TW K ++ S + + + +N LTIL E G YT V N LG+ V T V  
 Sbjct: 1270 TWMKFRKQIQDSEHIKVEN-ENGSKLTILAAARQEHGCGCYLLVENKLGSRQAQVNLT-V 1327

Query: 1248 LRKAERPSSSPCPDIGEVYADGVLLVWKPVESYGPVTYIVQCSLE----GGSWTTLASD 1302  
 + K + P+ +PC ++ + + L W SY + + S+E +W LA+  
 Sbjct: 1328 VDKPDPFAGTPCAS--DIRSSSLTLSWYG-SSYDGGSAVQSYSIEIWD SANKTWKELAT- 1383

Query: 1303 IFDCCYLTS----KLSRGGTYTFRACVSKAGMPYSSPSEQVLLGGP SHLAS----- 1351  
 C TS L Y FR ++ G S SE +G  
 Sbjct: 1384 ----CRSTSFNVQDLLPDHEYKFRVRRAINVTSEPSQSELT TVGEKPEEPKMKWRCQT 1439

Query: 1352 ----EESQGRSAQPLPSTKTFAF---QTQIQGRF SVVRQCWEKASGRALAAKIIP-YH 1403  
 E E R+ K F + ++ G+F V + EK + + A K Y  
 Sbjct: 1440 DDEKEPEVDYRTVTINTEQKVSDFYDIEERLGS GKFGVFR LVEKKTRK V WAGKFFKAYS 1499

Query: 1404 PKDKTAVLREYEALGLRHPHLAQLHAA YLSPRHLVLILELCSGPPELLP-CLAERASYSE 1462  
 K+K + +E + L HP L Q A+ ++V++LE+ SG EL + E +E  
 Sbjct: 1500 AKEKENIRQEISIMNCLHHPKLVQCVD AFEEKANIVMVLEIVSGGELFERIIDDFELTE 1559

Query: 1463 SEVKDYLWQMLSATQYLHNQHILHLDRSENMIITEY--NLLKVVDLGN AQSLSQE---K 1517  
 E Y+ Q+ +Y+H Q I+HLDL+ EN++ +K++D G A+ L K  
 Sbjct: 1560 RECIKYMRISEGVEYIHKQGI VHLDLKPENIMCVNKTGTRIKLIDFGLARLENAGSLK 1619

Query: 1518 VLPSPDKFKDYLETMAPELLEGQGA VPQTDIWAIGVTAFIMLSAEY PVSSEGARDLQRGLR 1577  
 VL E +APE++ + TD+W+IGV +I++S P + + +  
 Sbjct: 1620 VLFGTP-----EFVAPEVINYEPISYATDMWSIGVICYILVSGLS PFMGDNDNETLANVT 1674

Query: 1578 KGLVRL-SRCYAGLSGGAVAF LRSTLCAQPWGRPCASSCLQCPWLTEE 1624  
 + +S A F+ + L R + CLQ PWL ++  
 Sbjct: 1675 SATWDFDDEAFDEISDDAKDFISNLLKDMKNRLDCTQCLQHPWLMKD 1722 (SEQ ID NO:19)

Score = 64.4 bits (154), Expect = 9e-09  
 Identities = 36/106 (33%), Positives = 52/106 (48%), Gaps = 4/106 (3%)

Query: 54 PSMQVTIEDVQAQTGGTAQFEAIIEGDPQPSVTWYKDSVQLVDSTRLS-QQEGTTYSLV 112  
 P TI D++ G A+F+ IEG P P V W+KD + +S E SL+  
 Sbjct: 1808 PYFSKTIIRDLEVVEGSAARFDCKIEGYPDP EVVWFKDDQSIRESRHFQIDYDEDGNC SLI 1867

Query: 113 LRHVASKDAGVYTCLAQNTGGQVLCKAELLV---LGGDNEPDSEKQ 155  
 + V D YTC A N+ G+ C AEL+V G+ E + E++  
 Sbjct: 1868 ISDVCGD DDAKYTCKAVNSLGEATCTAELIVETMEEGE GEGE EEEEE 1913 (SEQ ID NO:20)

Score = 64.0 bits (153), Expect = 1e-08  
 Identities = 35/96 (36%), Positives = 46/96 (47%)

Query: 53 PPSMQVTIEDVQAQTGGTAQFEAIIEGDPQPSVTWYKDSVQLVDSTRLSQQEGTTYSLV 112  
 PP + V + G +F I G P QP VTW K +V L S R+S ++ L  
 Sbjct: 160 PPKFATKLG RVVKEGQMGRFSCKITGRPQPQVTWLKGNVPLQPSARVSVSEKNGMQVLE 219

Query: 113 LRHVASKDAGVYTCLAQNTGGQVLCKAELLVLGGDN 148  
 + V D G VYTCL N G+ AEL + G D+  
 Sbjct: 220 IHGVNQDDVG VYTCLVNVNGSGKASMSAELSIQGLDS 255 (SEQ ID NO:21)

Score = 59.3 bits (141), Expect = 3e-07  
 Identities = 30/100 (30%), Positives = 50/100 (50%), Gaps = 3/100 (3%)

Query: 47 LPALPGPPSMQVTIE---DVQAQTGGTAQFEAIIEGDPQPSVTWYKDSVQLVDSTRLSQQ 103  
 LP P P+ + ++ D++ G + G+P P V W + ++ +S +  
 Sbjct: 613 LVPAPSKPTAPIFLQLGLSDLKVMDSQVTMTVQVSGNPPPEVIWLHNGNEIQESED FHF 672

Query: 104 QEGTTYSLVLRHVASKDAGVYTCLAQNTGGQVLCKAELLV 143  
 Q GT +SL ++ V +D G YTC A N+ G+V +A L V  
 Sbjct: 673 QRGTHSLIQEVFPEDTGTYTCEAWNSAGEVRTQAVLTV 712 (SEQ ID NO:22)

FIGURE 2I

Docket No.: CL000927-CIP-DIV2

Serial No.: To b assigned

Inventors: Ming-Hui WEI et al.

Title: ISOLATED HUMAN KINASE PROTEINS...

Score = 57.4 bits (136), Expect = 1e-06  
Identities = 32/89 (35%), Positives = 46/89 (50%), Gaps = 1/89 (1%)

Query: 1160 PTFLRELSDETIVVLGQSVTLACQVSAQPAQAATWSKDGAPLESSSRVLISATLKNFQLLT 1219  
P F +L V GQ +C+++ +P Q TW K PL+ S+RV +S Q+L  
Sbjct: 161 PKFATKLGRVTVVKEGQMGFRFSCKITGRPQPQVTWLKGNVPLQPSARVSVSEK-NGMQVLE 219

Query: 1220 ILVVVAEDLGVTTCVSVSNALGTVTTTGVL 1248  
I V +D+GVYTC V N G + + L  
Sbjct: 220 IHGVNQDDVGVTCLVVNGSGKASMSAEL 248 (SEQ ID NO:23)

Score = 53.5 bits (126), Expect = 2e-05  
Identities = 32/98 (32%), Positives = 46/98 (46%), Gaps = 4/98 (4%)

Query: 1159 APTFLRELSDETIVVLGQSVTLACQVSAQPAQAATWSKDGAPLESSSRVLISATLKNFQLL 1218  
AP+F L D V+ GQ L C V P + TW +G P++ + + + L  
Sbjct: 513 APSFSSVLKDCAVIEGQDFVLQCSVRGTPVPRITWLLNGQPIQYARSTCEAGVAE----L 568

Query: 1219 TILVVVAEDLGVTTCVSVSNALGTVTTTGVLKRAERPSS 1256  
I + ED G YTC NALG V+ + + E+ SS  
Sbjct: 569 HIQDALPEDHGTYTCLAENALQVSCSAWVTVHEKKSS 606 (SEQ ID NO:24)

Score = 53.1 bits (125), Expect = 2e-05  
Identities = 37/113 (32%), Positives = 48/113 (41%), Gaps = 1/113 (0%)

Query: 1140 RKKPGLASFRLSGLKSWDRAPTFLRELSDETIVVLGQSVTLACQVSAQPAQAATWSKDGAP 1199  
+K + + L S AP FL+ LSD V+ G VT+ QVS P + W +G  
Sbjct: 603 KKSSRKSEYLLPVAPSKPTAPIFLQGLSDLKVMDSQVTMTVQVSGNPPPEVIWLHNGNE 662

Query: 1200 LESSSRVLISATLKNFQLLTILVVVAEDLGVTTCVSVSNALGTVTTTGVLKRAE 1252  
++ S L I V ED G YTC N+ G V T VL E  
Sbjct: 663 IQESEDHFHEQRTQHS-LWIEVFPEDTGTYTCEAWNSAGEVVRTQAVLTVQE 714 (SEQ ID NO:25)

Score = 51.9 bits (122), Expect = 5e-05  
Identities = 34/101 (33%), Positives = 50/101 (48%), Gaps = 2/101 (1%)

Query: 46 SLPALPGPPSMQVTIEDVQAQTGGTAQFEAIEGDPQPSVTWYKDSVQLVDSTR-LSQQQ 104  
S+P L P+ + ++ + G TA+FE + G P+P VTW+++ + R L  
Sbjct: 26 SMP-LTEAPAFILPPRNLCKIEGATAKFEGRVGRYPEPQVTWHRNGQPITSGGRFLLDG 84

Query: 105 EGTYSVLRLRHVASKDAGVYTCLAQNTGGQVLCKAELLVLG 145  
T+SLV+ V +D G YTC A N G EL V G  
Sbjct: 85 IRGTFSLVIHAVHEEDRGKYTCATNGSGARQVTVELTVEG 125 (SEQ ID NO:26)

Score = 50.8 bits (119), Expect = 1e-04  
Identities = 41/182 (22%), Positives = 65/182 (35%), Gaps = 26/182 (14%)

Query: 1130 PEGLEKEGPPRKKPGLASFRLSGLKSWDRA-----PTFLRELSDETV 1171  
P G E++ P +P R GL S D P F + + V  
Sbjct: 366 PSGEERKRPAPPRPATFTRQPLGSDVVSKAANRRIPMEGQRDSAFPKEKPSQSQEV 425

Query: 1172 VLQSVTLACQVSAQPAQAATWSKDGAPLESSSRVLISATLKNFQLLTILVVVAEDLGVT 1231  
Q+V C+VS P + W +G P+ + L +L D G Y  
Sbjct: 426 KENQTVKFRCEVSGIPKPEVAWFLEGTVPVRRQEGSIEVYEDAGSHYLCLLKARTRDSGT 485

Query: 1232 TCSVSNALGTVTTTGVLKRAERPSSSPCDIGEVYADGVLLVWKPVESYGPVTYIVQCSL 1291  
+C+ SNA G V+ + L+ P V D ++ + +++QCS+  
Sbjct: 486 SCTASNAQQVSCSWTLQVERLAVMEVAPSFSSVLKDCAVIEGQ-----DFVLQCSV 537

Query: 1292 EG 1293  
G  
Sbjct: 538 RG 539 (SEQ ID NO:27)

Score = 50.4 bits (118), Expect = 2e-04  
Identities = 26/100 (26%), Positives = 47/100 (47%), Gaps = 3/100 (3%)

FIGURE 2J

Docket No.: CL000927-CIP-DIV2  
Serial No.: To be assigned  
Inventors: Ming-Hui WEI et al.  
Title: ISOLATED HUMAN KINASE PROTEINS...

Query: 54 PSMQVTIEDVQAQTGGTAQFEAIIEGDPQPSVTWYKDSVQLVDSTRLSQQQEGTTYSLVL 113  
P+ + ++DV G + + DP ++ W + L + + QEG+ S+ +  
Sbjct: 1098 PAFKQKLQDVHVAEGKKLLQLQCQVSSDPPATIIWTLNGKTLKTTKFIILSQEGSLCSVSI 1157

Query: 114 RHVASKDAGVYTCLAQNTGGQVLCKAELLVLGGDNEPDSE 153  
+D G+Y C+A+N GQ C ++ V D+ P SE  
Sbjct: 1158 EKALLEDRGLYKCVAKNDAGQAECSCQVTV---DDAPASE 1194 (SEQ ID NO:28)

Score = 50.0 bits (117), Expect = 2e-04  
Identities = 35/125 (28%), Positives = 59/125 (47%), Gaps = 16/125 (12%)

Query: 1154 KSWDRAPTFLRELSDETIVLGGQSVTLACQVSAQPAQAATWSKDGAPLESSSRVLISATLK 1213  
+S AP F++L D V G+ + L CQVS+ P A W+ +G L+++ +++S  
Sbjct: 1092 ESQGTAPAFKQLQDVHVAEGKKLLQLQCQVSSDPPATIIWTLNGKTLKTTKFIILSQE-G 1150

Query: 1214 NFQLLTILVVVAEDLGVYTC-----SVSNALGTVTTTGVLRKAERPSSSP 1258  
+ ++I + ED G+Y C +V +A + T K+ RP SS  
Sbjct: 1151 SLCSVSIEKALLEDRGLYKCVAKNDAGQAECSCQVTVDDAPASENTKAPEMKSRPKSSL 1210

Query: 1259 CPDIG 1263  
P +G  
Sbjct: 1211 PPVLG 1215 (SEQ ID NO:29)

Score = 48.0 bits (112), Expect = 8e-04  
Identities = 26/87 (29%), Positives = 38/87 (42%)

Query: 1159 APTFLRELSDETIVLGGQSVTLACQVSAQPAQAATWSKDGAPLESSSRVLISATLKNFQLL 1218  
AP F+ + + G + +V P Q TW ++G P+ S R L+ ++ L  
Sbjct: 32 APAFILPPRNLCIKEGATAKFEGRVRGYPEPQVTWHRNGQPITSGGRFLDCGIRGTFSL 91

Query: 1219 TILVVVAEDLGVYTCSVSNALGTVTTT 1245  
I V ED G YTC +N G T  
Sbjct: 92 VIHAVHEEDRGKYTCEATNGSGARQVT 118 (SEQ ID NO:30)

Score = 45.3 bits (105), Expect = 0.005  
Identities = 37/140 (26%), Positives = 54/140 (38%), Gaps = 23/140 (16%)

Query: 22 TNHPSMVGCGWHPGLCGWGGGLHSSLPALPGPPSMQVTIEDVQAQTGGTAQFEAIIEGDP 81  
+N V C W + L + PS ++D G + + G P  
Sbjct: 490 SNAQQQVSCSWTLQV-----ERLAVMEVAPSFSSVLKDCAVIEGQDFVLQCSVRGTP 541

Query: 82 QPSVTWYKDS--VQLVDSTRLSQQQEGTTYSLVLRHVASKDAGVYTCLAQNTGGQVLCKA 139  
P +TW + +Q ST E L ++ +D G YTC+A+N GQV C A  
Sbjct: 542 VPRITWLLNGQPIQYARSTC-----EAGVAELHIQDALPEDHGTYTCLAENALGQVSCSA 596

Query: 140 ELLVLGGDNEPDSEKQSHRR 159  
+ V EK+S R+  
Sbjct: 597 WVTV-----HEKKSSRK 608 (SEQ ID NO:31)

Score = 44.5 bits (103), Expect = 0.009  
Identities = 26/104 (25%), Positives = 44/104 (42%), Gaps = 7/104 (6%)

Query: 41 GGLHSSLPALPGPPSMQVTIEDVQAQTGGTAQFEAIIEGDPQPSVTWYKDSVQLV-DSTR 99  
G S+ P P Q + + T +F + G P+P V W+ + +  
Sbjct: 407 GQRDSAPFKFESKPQSQ-----EVKENQTVKFRCEVSGIPKPEVAWFLEGTVPVRRQEGS 460

Query: 100 LSQQQEGTTYSLVLRHVASKDAGVYTCLAQNTGGQVLCKAELLV 143  
+ ++ ++ L L ++D+G Y+C A N GQV C L V  
Sbjct: 461 IEVYEDAGSHYLCLLKARTRDSGTYSCTASNAQQQVSCSWTLQV 504 (SEQ ID NO:32)

Score = 44.1 bits (102), Expect = 0.012  
Identities = 26/82 (31%), Positives = 38/82 (45%), Gaps = 1/82 (1%)

Query: 63 VQAQTGGTAQFEAIIEGDPQPSVTWYKDSVQLV-DSTRLSQQQEGTTYSLVLRHVASKDA 121

FIGURE 2K

Docket No.: CL000927-CIP-DIV2

Serial No.: To be assigned

Inventors: Ming-Hui WEI et al.

Title: ISOLATED HUMAN KINASE PROTEINS...

V A G + I GDP P+V W +D L D+ Q ++LVL+ V A  
Sbjct: 730 VTASLGQSVLISCAIAGDPFPTVHWRDGLCKDTGHFEVLQNEVDVFTLVLLKKVQPWHA 789

Query: 122 GVYTCLAQNTGGQVLCKAELLV 143  
G Y L +N G+ C+ L++  
Sbjct: 790 GQYEILLKNRVGECSCQVSLML 811 (SEQ ID NO:33)

Score = 43.8 bits (101), Expect = 0.015  
Identities = 26/89 (29%), Positives = 35/89 (39%)

Query: 1160 PTFLELSDETIVLGQSVTLACQVSAQPAQAATWSKDGAPLESSSRVLISATLKNFQLLT 1219  
P F + + D VV G + C++ P + W KD + S I L  
Sbjct: 1808 PYFSKTIRDLEVVEGSAARFDCKIEGYPDPEVVWFKDDQSIRESRHFQIDYDEDGNCSLI 1867

Query: 1220 ILVVVAEDLGVYTCSVSNALGTVTTTGV 1248  
I V +D YTC N+LG T T L  
Sbjct: 1868 ISDVCGDDDAKYTC KAVNSLGEATCTAEL 1896 (SEQ ID NO:34)

FIGURE 2L

Docket No.: CL000927-CIP-DIV2

Serial No.: To be assigned

Inventors: Ming-Hui WEI et al.

Title: ISOLATED HUMAN KINASE PROTEINS...

```
1 CAGCACGAGG AACTCCTTCT GATCACCTGG CCAGCTGAGG TCAGAGTGGG
51 AGAGGCAGTG GTTCCATTGA AGGAGTACTC CTAAGTGTCA GAAGCCTGGG
101 CGGTGAGGAT GGGGTGCTGT CGCTTGGGCT GCGGGGGGTG TTCAGTTGCC
151 CACAGTGTAT CTCAGGGTCT CACCAACCAT CCAAGCATGG TAGGCTGTGG
201 CTGGCACCCA GGGTGTGTG GCTGGGGAGG TGGTCTCCAC AGTTCCCTCC
251 CTGCCCTCCC AGGGCCCCCA TCCATGCAGG TAACCATCGA GGATGTGCAG
301 GCACAGACAG GCGGAACGGC CCAATTCGAG GCTATCATTG AGGGCGACCC
351 ACAGCCCTCG GTGACCTGGT ACAAGGACAG CGTCCAGCTG GTGGACAGCA
401 CCCGGCTTAG CCAGCAGCAA GAAGGCACCA CATACTCCCT GGTGCTGAGG
451 CATGTGGCCT CGAAGGATGC CGGCGTTTAC ACCTGCTGCG CCCAAAACAC
501 TGGTGGCCAG GTGCTCTGCA AGGCAGAGCT GCTGGTGCTT GGGGGGGACA
551 ATGAGCCGGA CTCAGAGAAG CAAAGCCACC GGAGGAAGCT GCACTCCTTC
601 TATGAGGTCA AGGAGGAGAT TGAAGGGGCG GTGTTTGGCT TCGTAAAAAG
651 AGTGACGACG AAAGGAAACA AGATCTTGTG CGCTGCCAAG TTCATCCCCC
701 TACGGAGCAG AACTCGGGCC CAGGCATACA GGGAGCGAGA CATCCTGGCC
751 GCGCTGAGCC ACCCGCTGGT CACGGGGCTG CTGGACCACT TTGAGACCCG
801 CAAGACCCTC ATCCTCATCC TGGAGCTGTG CTCATCCGAG GAGCTGCTGG
851 ACCGCCCTGA CAGGAAGGGC GTGGTGACGG AGGCCGAGGT CAAGGTCTAC
901 ATCCAGCAGC TGGTGGAGGG GCTGCACTAC CTGCACAGCC ATGGCGTTCT
951 CCACCTGGAC ATAAAGCCCT CTAACATCCT GATGGTGCAT CCTGCCCGGG
1001 AAGACATTAA AATCTGCGAC TTTGGCTTTG CCCAGAACAT CACCCAGCA
1051 GAGCTGCACT TCAGCCAGTA CGGCTCCCCT GAGTTCGTCT CCCCCGAGAT
1101 CATCCAGCAG AACCTGTGA GCGAAGCCTC CGACATTTGG GCCATGGGTG
1151 TCATCTCCTA CCTCAGCTG ACCTGCTCAT CCCCATTTGC CGGCGAGAGT
1201 GACCGTGCCA CCCTCCTGAA CGTCTGGAG GGGCGCGTGT CATGGAGCAG
1251 CCCCATGGCT GCCCACCTCA GCGAAGACGC CAAAGACTTC ATCAAGGCTA
1301 CGCTGCAGAG AGCCCTCAG GCCCGGCCCTA GTGCGGCCCA GTGCCCTCTC
1351 CACCCCTGGT TCCTGAAATC CATGCCTGCG GAGGAGGCCC ACTTCATCAA
1401 CACCAAGCAG CTCAGATTCC TCCTGGCCCG AAGTCGCTGG CAGCGTTCCC
1451 TGATGAGCTA CAAGTCCATC CTGGTGATGC GCTCCATCCC TGAGCTGTG
1501 CGGGGCCAC CCAGACAGCC CTCCCTCGGC GTAGCCCGGC ACCTCTGCAG
1551 GGACACTGGT GGCTCCTCCA GTTCTCTCTC CTCCTCTGAC AACGAGCTCG
1601 CCCCATTTGC CCGGGCTAAG TCACTGCCAC CCTCCCGGTG GACACACTCA
1651 CCACTGCTGC ACCCCCGGGG CTTCCTGCGG CCCTCGGCCA GCCTGCCTGA
1701 GGAAGCCGAG GCCAGTGAGC GCTCCACCGA GGCCCCAGCT CCGCTGCAT
1751 CTCCCAGGGG TGCCGGGCCA CCGGCCGCC AGGGCTGCGT GCCCGGCAC
1801 AGCGTCATCC GCAGCCTGTT CTACCACAG GCGGGTGAGA GCCCTGAGCA
1851 CGGGGCCCTG GCCCGGGGA GCAGGCGGCA CCCGGCCCG CGGCGGCACC
1901 TGCTGAAGGG CGGTACATT GCGGGGCGCG TGCCAGGCCT GCGCGAGCCA
1951 CTGATGAGC ACCGCGTGTG GGAGGAGGAG GCCGCCAGG AGGAGCAGGC
2001 CACCCCTCTG GCCAAAGCCC CCTCATTCGA GACTGCCCTC CGGCTGCCTG
2051 CCTCTGGCAC CCACTTGGCC CTTGGCCACA GCCACTCCCT GGAACATGAC
2101 TCTCCGAGCA CCCCCCGCCC CTCTCGGAG GCCTGCGGTG AGGCACAGCG
2151 ACTGCCTTCA GCCCCTCCG GGGGGGCCCC TATCAGGGAC ATGGGGCACC
2201 CTCAGGGCTC CAAGCAGCTT CCATCCACTG GTGGCCACCC AGGCACTGCT
2251 CAGCCAGAGA GGCCATCCCC GGACAGCCCT TGGGGGCAGC CAGCCCTTT
2301 CTGCCACCCC AAGCAGGGTT CTGCCCCCA GGAGGGCTGC AGCCCCCACC
2351 CAGCAGTTGC CCCATGCCCT CTGGCTCCT TCCCTCCAGG ATCTTGCAAA
2401 GAGGCCCCCT TAGTACCCTC AAGCCCCCTC TTGGGACAGC CCCAGGCACC
2451 CCCTGCCCTT GCCAAAGCAA GCCCCCCATT GGAATCTAAG ATGGGGCCTG
2501 GAGACATCTC TCTTCTGGG AGGCCAAAAC CCGGCCCTG CAGTTCCCCA
2551 GGGTCAGCCT CCCAGGCGAG CTCTTCCCA GTGAGTCCC TCAGGTGGG
2601 CTCCTCCAG GTGGGCACAG AGCCTGGCCC CTCCCTGGAT GCGGAGGGCT
2651 GGACCCAGGA GGCTGAGGAT CTGTCCGACT CCACACCCAC CTGACAGCGG
2701 CCTCAGGAAC AGGTGACCAT GCGCAAGTTC TCCTTGGGTG GTCGCGGGG
2751 CTACGAGGC GTGGCTGGCT ATGGCACCTT TGCCTTTGGT GGAGATGCAG
2801 GGGGCATGCT GGGGCAGGGG CCCATGTGGG CCAGGATAGC CTGGGCTGTG
2851 TCCCAGTCGG AGGAGGAGGA GCAGGAGGAG GCCAGGGCTG AGTCCCAGTC
2901 GGAGGAGCAG CAGGAGGCCA GGGCTGAGAG CCCACTGCCC CAGGTCACTG
2951 CAAGGCCTGT GCCTGAGGTC GGCAGGGCTC CCACAGGAG CTCTCCAGAG
3001 CCCACCCCAT GGGAGGACAT CCGGCAGGTC TCCCTGGTGC AGATCCGGGA
3051 CCTGTGAGGT GATGCGGAGG CGGCCGACAC AATATCCCTG GACATTTCCG
3101 AGGTGAGACC CGCTACCTC AACCTCTCAG ACCTGTACGA TATCAAGTAC
3151 CTCCCATTCG AGTTTATGAT CTTAGGAAA GTCCCCAAGT CCGCTCAGCC
3201 AGAGCCGCCC TCCCCATGG CTGAGGAGGA GCTGGCCGAG TTCCCGGAGC
3251 CCACGTGGCC CTGGCCAGGT GAACTGGGCC CCCACGCAGG CCTGGAGATC
3301 ACAGAGGAGT CAGAGGATGT GGACGCGCTG CTGGCAGAGG CTGCCGTGGG
3351 CAGGAAGCGC AAGTGGTCCT CGCCGTACAG CAGCCTCTTC CACTTCCCTG
3401 GGAGGCACCT GCCGCTGGAT GAGCCTGCAG AGCTGGGGCT GCGTGAGAGA
3451 GTGAAGGCCT CCGTGAGCA CATCTCCCG ATCCTGAAGG GCAGGCCGGA
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FIGURE 3A

Docket No.: CL000927-CIP-DIV2

Serial No.: To b assigned

Inventors: Ming-Hui WEI et al.

Title: ISOLATED HUMAN KINASE PROTEINS...

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3501 AGGTCTGGAG AAGGAGGGGC CCCCAGGAA GAAGCCAGGC CTGCTTCCT
3551 TCCGGCTCTC AGGTCTGAAG AGCTGGGACC GAGCGCCGAC ATTCCTAAGG
3601 GAGCTCTCAG ATGAGACTGT GGTCTGGGC CAGTCAGTGA CACTGGCCTG
3651 CCAGGTGTCA GCCCAGCCAG CTGCCCAGGC CACCTGGAGC AAAGACGGAG
3701 CCCCCCTGGA GAGCAGCAGC CGTGTCTCA TCTCTGCCAC CCTCAAGAAC
3751 TTCCAGTTC TGACCATCCT GGTGGTGGTG GCTGAGGACC TGGGTGTGTA
3801 CACCTGCAGC GTGAGCAATG CGCTGGGGAC AGTGACCACC ACGGGCGTCC
3851 TCCGGAAGGC AGAGCGCCCC TCATCTTCGC CATGCCCGGA TATCGGGGAG
3901 GTGTACGCGG ATGGGGTGCT GCTGGTCTGG AAGCCCGTGG AATCCTACGG
3951 CCCTGTGACC TACATTGTGC AGTGCAGCCT AGAAGGCGGC AGCTGGACCA
4001 CACTGGCCTC CGACATCTTT GACTGCTGCT ACCTGACCAG CAAGCTCTCC
4051 CGGGGTGGCA CCTACACCTT CCGCACGGCA TGTGTCAGCA AGGCAGGAAT
4101 GGGTCCCGAG AGCAGCCCCC CGGAGCAAGT CCTCCTGGGA GGGCCAGCC
4151 ACCTGGCCTC TGAGGAGGAG AGCCAGGGGC GGTGAGCCCA ACCCCTGCCC
4201 AGCACAAGA CTTTCGCATT CCAGACACAG ATCCAGAGGG GCCGCTTCAG
4251 CGTGGTGGCG CAATGTGGG AGAAGGCCAG CGGGCGGGCG CTGGCCGCCA
4301 AGATCATCCC CTACCACCCC AAGGACAAGA CAGCAGTGCT GCGCGAATAC
4351 GAGGCCCTCA AGGGCCTGCG CCACCCGCAC CTGGCCAGC TGCACGCAGC
4401 CTACCTCAGC CCCCAGCACC TGGTGCTCAT CTTGGAGCTG TGCTCTGGGC
4451 CCAGAGTGCT CCCCTGCCTG GCCGAGAGGG CCTCCTACTC AGAATCTGAG
4501 GTGAAGGACT ACCTGTGGCA GATGTTGAGT GCCACCCAGT ACCTGCACAA
4551 CCAGCACATC CTGCACCTGG ACCTGAGGTC CGAGAACATG ATCATACCG
4601 AATACAACCT GCTCAAGGTC GTGGACCTGG GCAATGCACA GAGCCTCAGC
4651 CAGGAGAAGG TGCTGCCCTC AGACAAGTTC AAGGACTACC TAGAGACCAT
4701 GGTCCAGAG TCTCTGGAGG GCCAGGGGGC TGTTCCACAG ACAGACATCT
4751 GGGCCATCGG TGTGACAGCC TTCATCATGC TGAGCGCCGA GTACCCGGTG
4801 AGCAGCGAGG GTGCACGCGA CCTGCAGAGA GGAATGCGCA AGGGGCTGGT
4851 CCGGCTGAGC CGCTGTACG CGGGGCTGTC CGGGGGCGCC GTGGCCTTCC
4901 TGCGCAGCAC TCTGTGCGCC CAGCCCTGGG GCCGGCCCTG CGCGTCCAGC
4951 TGCCTGCAGT GCCCGTGGCT AACAGAGGAG GGCCCGGCCT GTTCGCGGCC
5001 CGCGCCCGTG ACCTTCCCTA CCGCGCGGCT GCGCGTCTTC GTGCGCAATC
5051 GCGAGAAGAG ACGCGCGCTG CTGTACAAGA GGCACAACCT GGCCAGGTG
5101 CGCTGAGGGT CGCCCCGGCC ACACCCTTGG TCTCCCCGCT GGGGGTCGCT
5151 GCAGACGCGC CAATAAAAC GCACAGCCGG GCGAGAAAAA AAAAAAAAAA
5201 AAAAAA (SEQ ID NO:3)
```

**FEATURES:**

Start: 109  
Exon: 109-5103  
Stop: 5104

**SNPs:**

DNA				Protein		
Position	Major	Minor	Domain	Position	Major	Minor
311	T	C G	Exon	68	V	A G
1741	C	T	Exon	545	P	S
2714	T	C	Exon	869	V	A
2745	C	T	Exon	879	R	R
2859	A	G	Exon	917	S	S
3420	T	C	Exon	1104	D	D

**Context:**

DNA  
Position

```
311 AACTCCTTCTGATCACCTGGCCAGCTGAGGTCAGAGTGGGAGAGGCAGTGGTTCATTGA
AGGAGTACTCCTAACTGTCAGAAGCCTGGGCGGTGAGGATGGGGTGCTGTCGCTTGGGCT
GCGGGGGGTGTTTCAGTTGCCACAGTGTATCTCAGGGTCTCACCAACCATCAAGCATGG
TAGGCTGTGGCTGGCACCCAGGGTTGTGTGGCTGGGAGGTGGTCTCCACAGTTCCTCC
CTGCCCTCCAGGGCCCCCATCCATGCAGGTAACCATCGAGGATGTGCAGGCACAGACAG
[T, C, G]
CGGAACGGCCCCAATTTCGAGGCTATCATGAGGGCGACCCACAGCCCTCGGTGACCTGGTA
CAAGGACAGCGTCCAGTGGTGGACAGCACCCGGCTTAGCCAGCAGCAAGAAGGCACCAC
ATACTCCCTGGTCTGAGGCATGTGGCTCGAAGGATGCCGGCGTTTACACCTGCCCTGGC
CCAAAACACTGGTGGCCAGGTGCTCTGCAAGGCAGAGCTGCTGGTGTCTGGGGGGGACAA
TGAGCCGGACTCAGAGAAGCAAAGCCACCGGAGGAAGCTGCACTCCTTCTATGAGGTCAA
```

FIGURE 3B



Docket No.: CL000927-CIP-DIV2  
Serial No.: To be assigned  
Inventors: Ming-Hui WEI et al.  
Title: ISOLATED HUMAN KINASE PROTEINS...

1741 CAGCGTTCCCTGATGAGCTACAAGTCCATCCTGGTGATGCGCTCCATCCCTGAGCTGCTG  
CGGGGCCACCCGACAGCCCTCCCTCGGCGTAGCCCGGCACCTCTGCAGGGACACTGGT  
GGCTCCTCCAGTTCTCTCCTCCTCTGACAACGAGCTCGCCCCATTGCCCCGGGCTAAG  
TCACTGCCACCCTCCCCGGTGACACACTCACCCTGCTGCACCCCCGGGGCTTCTGCGG  
CCCTCGGCGAGCTGCTGAGGAAGCCGAGGCCAGTGAGCGCTCCACCGAGGCCAGCT  
[C, T]  
CGCCTGCATCTCCCGAGGGTGCCGGGCCACCGGCCCGCCAGGGCTGCGTGCCCCGGCACA  
GCGTCATCCGAGCCTGTTCTACCACAGGCGGGTGAGAGCCCTGAGCACGGGGCCCTGG  
CCCCGGGGAGCAGGCGGCACCCGGCCCGCGCGGCACCTGCTGAAGGGCGGCTACATG  
CGGGGCGCTGCCAGGCTGCGCGAGCCACTGATGGAGCACCGCTGCTGGAGGAGGAGG  
CCGCGAGGAGGAGCAGGCCACCTCCTGGCCAAAGCCCCCTATTGAGACTGCCCTCC

2714 TACCCTCAAGCCCTTCTTGGGACAGCCCCAGGCACCCCTGCCCCTGCCAAAGCAAGCC  
CCCCATTGAGCTCTAAGATGGGGCCTGGAGACATCTCTTCTTCTGGGAGGCCAAAACCCG  
GCCCTGTCAGTTCCCGAGGGTCAGCCTCCAGGCGAGCTCTTCCCAAGTGAGCTCCCTCA  
GGTGGGCTCCTCCAGGTGGGCACAGAGCCTGGCCCCCTCCCTGGATGCGGAGGGCTGGA  
CCAGGAGGCTGAGGATCTGTCCGACTCCACACCCACCTTGACGCGGCTCAGGAACAGG  
[T, C]  
GACCATGCGCAAGTTCTCCCTGGGTGGTTCGCGGGGGCTACGCAGGCGTGGCTGGCTATGG  
CACCTTTGCCCTTGGTGGAGATGCAGGGGGCATGCTGGGGCAGGGGCCATGTGGGCCAG  
GATAGCCTGGGGTGTGTCCAGTCGGAGGAGGAGGAGCAGGAGGAGGCCAGGGCTGAGTC  
CCAGTCGGAGGAGCAGCAGGAGGCCAGGGCTGAGAGCCACTGCCCCAGGTGAGTCAAG  
GCCTGTGCTGAGGTGCGCAGGGCTCCACAGGAGCTCTCCAGAGCCACCCATGGGA

2745 GGCACCCCTGCCCCTGCCAAAGCAAGCCCCCATTGGACTCTAAGATGGGGCCTGGAGA  
CATCTCTCTTCTGGGAGGCCAAAACCCGGCCCTGCAGTTCCCGAGGGTCAGCCTCCCA  
GGCGAGCTCTTCCCAAGTGAGCTCCCTCAGGGTGGGCTCCTCCAGGTGGGCACAGAGCC  
TGGCCCCCTCCCTGGATGCGGAGGGCTGGACCCAGGAGGCTGAGGATCTGTCCGACTCCAC  
ACCCACCTTGACGCGCCTCAGGAACAGGTGACCATGCGCAAGTTCTCCCTGGGTGGTTCG  
[C, T]  
GGGGGCTACGCAGGCGTGGCTGGCTATGGCACCTTTGCCTTTGGTGGAGATGCAGGGGGC  
ATGCTGGGGCAGGGGCCATGTGGGCCAGGATAGCCTGGGCTGTGTCCAGTCGGAGGAG  
GAGGAGCAGGAGGAGGCCAGGGCTGAGTCCAGTCGGAGGAGCAGCAGGAGGCCAGGGCT  
GAGAGCCACTGCCCCAGGTGAGTGAAGGCCTGTGCCTGAGGTGCGCAGGGCTCCACC  
AGGAGCTCTCCAGAGCCACCCATGGGAGGACATCGGGCAGGTCTCCCTGGTGCGATC

2859 CTCCCAGGCGAGCTCTTCCCAAGTGAGCTCCCTCAGGGTGGGCTCCTCCAGGTGGGCAC  
AGAGCCTGGCCCTCCTGGATGCGGAGGGCTGGACCCAGGAGGCTGAGGATCTGTCCGA  
CTCCACACCCACCTTGACGCGCCTCAGGAACAGGTGACCATGCGCAAGTTCTCCCTGGG  
TGCTGCGGGGGCTACGCAGGCGTGGCTGGCTATGGCACCTTTGCCTTTGGTGGAGATGC  
AGGGGGCATGTGGGGCAGGGGCCATGTGGGCCAGGATAGCCTGGGCTGTGTCCAGTC  
[A, G]  
GAGGAGGAGGAGCAGGAGGAGGCCAGGGCTGAGTCCAGTCGGAGGAGCAGCAGGAGGCC  
AGGGCTGAGAGCCACTGCCCCAGGTGAGTGAAGGCCTGTGCCTGAGGTGCGCAGGGCT  
CCCACAGGAGCTCTCCAGAGCCACCCATGGGAGGACATCGGGCAGGTCTCCCTGGTG  
CAGATCCGGGACCTGTGAGGTGATGCGGAGGCGGCCGACACAATATCCCTGGACATTTCC  
GAGGTGGACCCCGCTACCTCAACCTCTCAGACCTGTACGATATCAAGTACCTCCCATTC

3420 CAACCTCTCAGACCTGTACGATATCAAGTACCTCCCATTCGAGTTTATGATCTTCAGGAA  
AGTCCCCAAGTCCGCTCAGCCAGAGCCGCTCCCCATGGCTGAGGAGGAGCTGGCCGA  
GTTCCCGAGCCACGTGGCCCTGGCCAGGTGAAGTGGGCCCCACGCAGGCTGGAGAT  
CACAGAGGAGTCAGAGGATGTGGACGCGCTGCTGGCAGAGGCTGCCGTGGGCAGGAAGCG  
CAAGTGGTCTCGCCGTCACGCAGCTCTTCCACTTCCCTGGGAGGCACCTGCCGCTGGA  
[T, C]  
GAGCCTGCAGAGCTGGGGCTGCGTGAGAGAGTGAAGGCCTCCGTGGAGCACATCTCCCGG  
ATCCTGAAGGGCAGGCCGGAAGGTCTGGAGAAGGAGGGGCCCCCAGGAAGAAGCCAGGC  
CTTGCTTCTCCTCCGGCTCTCAGGTCTGAAGAGCTGGGACCGAGCGCCGACATTCCTAAGG  
GAGCTCTCAGATGAGACTGTGGTCTTGGGCCAGTCAGTGACACTGGCCTGCCAGGTGTCA  
GCCAGCCAGCTGCCAGGCCACCTGGAGCAAAGACGAGGCCCCCCCTGGAGAGCAGCAGC

Chromosome map position: 1

Bac accession number: AC023889

FIGURE 3C